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Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Keisha Douglas
Timestamp: [year=2009; month=1; day=22; hr=16; min=26; sec=44; ms=514;]
=====

Reviewer Comments:

<210> 56

<211> 17752

<212> DNA

<213> Phaeodactylum tricornutum, Physcomitrella patens

<210> 71

<211> 17061

<212> DNA

<213> Phaeodactylum tricornutum, Physcomitrella patens, Caenorhabditis
elegans

The above <213> responses for sequence id#'s 56 and 71 are both
invalid, only one organism response is allowed for this line.

<210> 100

<211> 25

<212> DNA

<213> unknown

<220>

<221> misc_feature

<222> (1)..(25)

<223> ACtrau-5'

<210> 103

<211> 22
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(22)
<223> YES-HIS-5'

Please explain the above <223> responses for sequence id#s 100 and 103.
FYI, please do not use foreign language in U.S. applications. Please
correct the remaining sequences showing similar errors.

Application No: 10552013

Version No: 2.0

Input Set:

Output Set:

Started: 2009-01-07 16:25:11.916

Finished: 2009-01-07 16:25:23.759

Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 843 ms

Total Warnings: 109

Total Errors: 51

No. of SeqIDs Defined: 148

Actual SeqID Count: 148

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (28)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)
W 402	Undefined organism found in <213> in SEQ ID (31)
W 402	Undefined organism found in <213> in SEQ ID (32)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (52)
W 213	Artificial or Unknown found in <213> in SEQ ID (53)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (53)
W 213	Artificial or Unknown found in <213> in SEQ ID (54)

Input Set:

Output Set:

Started: 2009-01-07 16:25:11.916
Finished: 2009-01-07 16:25:23.759
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 843 ms
Total Warnings: 109
Total Errors: 51
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (54)
W 213	Artificial or Unknown found in <213> in SEQ ID (55)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (55)
W 402	Undefined organism found in <213> in SEQ ID (56)
W 402	Undefined organism found in <213> in SEQ ID (57)
W 402	Undefined organism found in <213> in SEQ ID (58)
W 402	Undefined organism found in <213> in SEQ ID (59)
W 213	Artificial or Unknown found in <213> in SEQ ID (60)
W 213	Artificial or Unknown found in <213> in SEQ ID (61)
W 213	Artificial or Unknown found in <213> in SEQ ID (62)
W 213	Artificial or Unknown found in <213> in SEQ ID (63)
W 213	Artificial or Unknown found in <213> in SEQ ID (64)
W 213	Artificial or Unknown found in <213> in SEQ ID (65)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (65)
W 213	Artificial or Unknown found in <213> in SEQ ID (66)
W 213	Artificial or Unknown found in <213> in SEQ ID (67)
W 213	Artificial or Unknown found in <213> in SEQ ID (68)
W 402	Undefined organism found in <213> in SEQ ID (71)
W 402	Undefined organism found in <213> in SEQ ID (72) This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (75)

Input Set:

Output Set:

Started: 2009-01-07 16:25:11.916
Finished: 2009-01-07 16:25:23.759
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 843 ms
Total Warnings: 109
Total Errors: 51
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (75)
W 213	Artificial or Unknown found in <213> in SEQ ID (76)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (76)
W 213	Artificial or Unknown found in <213> in SEQ ID (77)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (77)
W 213	Artificial or Unknown found in <213> in SEQ ID (78)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (78)
W 213	Artificial or Unknown found in <213> in SEQ ID (79)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (79)
W 213	Artificial or Unknown found in <213> in SEQ ID (80)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (80)
W 213	Artificial or Unknown found in <213> in SEQ ID (81) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (81)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (82)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (83)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (84)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (85)

Input Set:

Output Set:

Started: 2009-01-07 16:25:11.916
Finished: 2009-01-07 16:25:23.759
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 843 ms
Total Warnings: 109
Total Errors: 51
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (86)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (87)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (88)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (89) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Renz, Andreas
 Sozer, Nursen
 Frentzen, Margit
 Bauer, Jorg
 Keith, Stobart
 Fraser, Thomas
 Lazarus, Colin M
 Qi, Baoxiu
 Abbadi, Amine
 Heinz, Ernst

<120> NOVEL PLANT ACYLTRANSFERASES SPECIFIC FOR LONG-CHAINED, MULTIPLY
 UNSATURATED FATTY ACIDS

<130> 13478-00002-US

<140> 10552013
 <141> 2005-09-30

<150> PCT/EP2004/003224
 <151> 2004-03-26

<150> DE103 14 759.4
 <151> 2003-03-31

<150> DE103 48 996.7
 <151> 2003-10-17

<160> 148

<170> PatentIn version 3.3

<210> 1
 <211> 1047
 <212> DNA
 <213> Thraustochytrium

<220>
 <221> CDS
 <222> (38)..(952)
 <223> LPAAT

<400> 1

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 1 5

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 Ala Lys Thr Ala Val Gly Leu Leu Thr Leu Ala Pro Ala Arg Ile Val
 10 15 20

ttc ctc gtg act gtc ctg ggc acg tac ggg ctc acg gtc gcg gcc tgc 151
 Phe Leu Val Thr Val Leu Gly Thr Tyr Gly Leu Thr Val Ala Ala Cys
 25 30 35

acg cga ctt ggc gtc ccg aaa agc ttc gtg ctg ggc ctg acg cgg tgc 199

Thr Arg Leu Gly Val Pro Lys Ser Phe Val Leu Gly Leu Thr Arg Cys
 40 45 50
 gtc gcg cga ctc acg ctc tgg ggg ctt ggg ttc tac cac att gag gtc 247
 Val Ala Arg Leu Thr Leu Trp Gly Leu Gly Phe Tyr His Ile Glu Val
 55 60 65 70
 tct tgc gac gcc caa ggc ctt cgg gag tgg cgg cgc gtg att gtc gcg 295
 Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp Pro Arg Val Ile Val Ala
 75 80 85
 aac cac gtc tcg tac ctg gag atc ttg tac ttc atg tcg acc gtg cac 343
 Asn His Val Ser Tyr Leu Glu Ile Leu Tyr Phe Met Ser Thr Val His
 90 95 100
 tgc cgg tct ttc gtc atg aag aag acc tgc ctc cga gtc cgg ctt gtc 391
 Cys Pro Ser Phe Val Met Lys Lys Thr Cys Leu Arg Val Pro Leu Val
 105 110 115
 ggc tac att gcc atg gag ctg ggc ggt gtg att gtg gac cgc gag ggc 439
 Gly Tyr Ile Ala Met Glu Leu Gly Gly Val Ile Val Asp Arg Glu Gly
 120 125 130
 ggc ggt caa agc gca tcg gcg atc att cgc gac cgc gtg cag gag cct 487
 Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg Asp Arg Val Gln Glu Pro
 135 140 145 150
 cct cga gat tcg tcg agc gag aag cac cac gcg cag cgg ctt ctt gtg 535
 Pro Arg Asp Ser Ser Ser Glu Lys His His Ala Gln Pro Leu Leu Val
 155 160 165
 ttc ccc gag ggg acc acc acc aat gga agc tgc ctg ctc caa ttc aag 583
 Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser Cys Leu Leu Gln Phe Lys
 170 175 180
 acg gga gcc ttt cgt cct ggg gct cgg gtg ctt cgg gtc gtg ctt gag 631
 Thr Gly Ala Phe Arg Pro Gly Ala Pro Val Leu Pro Val Val Leu Glu
 185 190 195
 ttt ccg att gac aaa gcg cgt ggt gac ttt tcc ccg gcg tac gaa tcg 679
 Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe Ser Pro Ala Tyr Glu Ser
 200 205 210
 gtc cac acg cca gct cac ctc ctt cgc atg ctc gca caa tgg agg cac 727
 Val His Thr Pro Ala His Leu Leu Arg Met Leu Ala Gln Trp Arg His
 215 220 225 230
 cgg ctt cgg gtg cgc tat ctt cct ctg tat gag ccc tct gcg gct gag 775
 Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr Glu Pro Ser Ala Ala Glu
 235 240 245
 aag gtt gat gca gac ctt tat gcg cgg aac gtg cgc gac gaa atg gcg 823
 Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn Val Arg Asp Glu Met Ala
 250 255 260
 cgc gcg ctc aag gta ccc act gtg gag cag tct tac cgc gac aag ctc 871
 Arg Ala Leu Lys Val Pro Thr Val Glu Gln Ser Tyr Arg Asp Lys Leu
 265 270 275
 gtc tac cac gcg gat ctc atg cgg cac tac cag aag gcc ggc ccc gga 919
 Val Tyr His Ala Asp Leu Met Pro His Tyr Gln Lys Ala Gly Pro Gly
 280 285 290
 gcg ctc tat ctg tac gtc cga cct gac ctc ttg tagcaactcat gcgcgtccca 972
 Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu Leu
 295 300 305
 agcgggtccag caacgggaga ttaaaacacg atttcttagc ctacaaaaaa aaaaaaaaaa 1032
 aaaaaaaaaa aaaaaa 1047

<210> 2

<211> 305

<212> PRT

<213> Thraustochytrium

<400> 2

Met Ser Ala Trp Thr Arg Ala Lys Thr Ala Val Gly Leu Leu Thr Leu
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Ala Pro Ala Arg Ile Val Phe Leu Val Thr Val Leu Gly Thr Tyr Gly
20 25 30
Leu Thr Val Ala Ala Cys Thr Arg Leu Gly Val Pro Lys Ser Phe Val
35 40 45
Leu Gly Leu Thr Arg Cys Val Ala Arg Leu Thr Leu Trp Gly Leu Gly
50 55 60
Phe Tyr His Ile Glu Val Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp
65 70 75 80
Pro Arg Val Ile Val Ala Asn His Val Ser Tyr Leu Glu Ile Leu Tyr
85 90 95
Phe Met Ser Thr Val His Cys Pro Ser Phe Val Met Lys Lys Thr Cys
100 105 110
Leu Arg Val Pro Leu Val Gly Tyr Ile Ala Met Glu Leu Gly Gly Val
115 120 125
Ile Val Asp Arg Glu Gly Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg
130 135 140
Asp Arg Val Gln Glu Pro Pro Arg Asp Ser Ser Ser Glu Lys His His
145 150 155 160
Ala Gln Pro Leu Leu Val Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser
165 170 175
Cys Leu Leu Gln Phe Lys Thr Gly Ala Phe Arg Pro Gly Ala Pro Val
180 185 190
Leu Pro Val Val Leu Glu Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe
195 200 205
Ser Pro Ala Tyr Glu Ser Val His Thr Pro Ala His Leu Leu Arg Met
210 215 220
Leu Ala Gln Trp Arg His Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr
225 230 235 240
Glu Pro Ser Ala Ala Glu Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn
245 250 255
Val Arg Asp Glu Met Ala Arg Ala Leu Lys Val Pro Thr Val Glu Gln
260 265 270
Ser Tyr Arg Asp Lys Leu Val Tyr His Ala Asp Leu Met Pro His Tyr
275 280 285
Gln Lys Ala Gly Pro Gly Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu
290 295 300
Leu
305

<210> 3

<211> 1701

<212> DNA

<213> Physcomitrella patens

<220>

<221> misc_feature

<223> LPAAT

<400> 3

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aggtatgtct tattaatgaa aatgtctcca cacatgtatg ttgttttagt atattctgtc 120
aagcgaacac ttgttttaatt tttttcttaa attgaaatc ttgtgctgaa agccaaactc 180
aggtccatca taatgtagca atatgatcag aagcgctcaa atgtgtcgtg aaagtttgct 240
tttgcaattt tcttttctgt ttaacctatt gattatgttg gaaccacaa acagacgctg 300
cttcactcca tctctatggt aatgaatgct gtgatgatc cggtaattt catcctacag 360
ggatatggat gttgtaagg tgatttttgc aggtgataaa gtacctaagg agaaccgtgt 420
gatggctcat tgcaaccatc gtaccgaagt ggactggatg tacatttga acttagcaat 480
tcggaaaggg aagattgggt actgcaagta tgcggtgaa aactcagtga aaaacttacc 540
cttgtttggt tgggcatttt acgtttttga gtttctgatg ctgcataaaa agtgggaagt 600
ggatgctccc gcatcaaga catacattga cagttttcaa gataaaaagag atcctctctg 660
gctagtctgt tttctgaag gcacagattt ttctgaagg tgaaagtacc atccatggct 720
ttgatgtata tctgcaatct tctctataat ctgcatttat tctctgtgt tctctagca 780
agtaaatcat acttgcttaa tgtacttagc aatttgcct ttttgacta ttgtgatgta 840
aatgtgattg actactatga cagtgaagcg aaacgggaca cgggcaatgc aattggaaga 900
gagaaaggct atccggagct tgtcaatgtg cttcaacctc gcaactcgtg ctttgtact 960
tgcccttctc aatcgctgctg ctctttggat gcagtttatg acctcactat agggtaacag 1020
aagcgggtgc ccttgttcat caacaatgta ttccgaaccg atccatcgga agtgccactt 1080
cacattcgcc gaatccaat tctgagatt cctcaatcag aagacggatg gacgcagttg 1140
ctgtatgatc tattttatca aaaggaccag atgttgcca gttttagtaa gacaggtcct 1200
ttccctgaca gtggaaattga agagagccct ttgaacatag tggaaagggt ttgcaattgt 1260
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cctaaccggg ttactctag tctacgtact aaaagaaaaa tcgtgtaaaa taaattcgtt 1440
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atacggttgt cttctctgta tgaacctcag tgcttcaaga cgaatgtggcc ttttagcctt 1620
ctcctttacc catcttgacc agatgccaaa ctgcataaa agcagatcaa taggtcgtgc 1680
cccaaaaaaa aaaaaaaaaa a 1701

<210> 4

<211> 714

<212> DNA

<213> *Physcomitrella patens*

<220>

<221> CDS

<222> (1)..(714)

<223> LPAAT

<400> 4

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Met Ala Leu Met Tyr Ile Cys Asn Leu Leu Tyr Asn Leu His Leu Phe
1 5 10 15
tct gtt gtt tct cta gca agt aaa tca tac ttg ctt aat gta ctt agc 96
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
20 25 30
aat ttg tca ttt ttg act tat tgt gat gta aat gtg att gac tac tat 144
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr

35	40	45	
gac agt gaa gcg aaa cgg gac acg ggc aat gca att gga aga gag aaa			192
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys			
50	55	60	
ggc tat ccg gag ctt gtc aat gtg ctt caa cct cgc act cgt ggc ttt			240
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe			
65	70	75	80
gtg act tgc ctt tct caa tcg cgc tgc tct ttg gat gca gtt tat gac			288
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp			
85	90	95	
ctc act ata ggg tac aag aag cgg tgt ccc ttg ttc atc aac aat gta			336
Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val			
100	105	110	
ttc gga acc gat cca tcg gaa gtg cac att cac att cgc cga ata cca			384
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro			
115	120	125	
att tct gag att cct caa tca gaa gac ggt atg acg cag tgg ctg tat			432
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr			
130	135	140	
gat cta ttt tat caa aag gac cag atg ttg gcc agt ttt agt aag aca			480
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr			
145	150	155	160
ggc tct ttc cct gac agt gga att gaa gag agc cct ttg aac ata gtg			528
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val			
165	170	175	
gaa ggt gtt tgc aat gtt gct cta cac gta gtc ctt agc ggt tgg gta			576
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val			
180	185	190	
ttc tgg tgc ttg ttt cat tcg gtt tgg ttg aag ctt tat gtg gct ttc			624
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe			
195	200	205	
gct agt ttg ctg ctc gcg ttt agt acc tat ttt gat tgg aga cct aaa			672
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys			
210	215	220	
ccg gtt tac tct agt cta cgt act aaa aga aaa atc gtg taa			714
Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val			
225	230	235	

<210> 5

<211> 237

<212> PRI

<213> Physcomitrella patens

<400> 5

Met Ala Leu Met Tyr Ile Cys Asn Leu Leu Tyr Asn Leu His Leu Phe		
1	5	10
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser		
20	25	30
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr		
35	40	45
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys		
50	55	60

Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
 65 70 75 80
 Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
 85 90 95
 Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
 100 105 110
 Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
 115 120 125
 Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
 130 135 140
 Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
 145 150 155 160
 Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
 165 170 175
 Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
 180 185 190
 Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
 195 200 205
 Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
 210 215 220
 Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
 225 230 235

<210> 6

<211> 507

<212> DNA

<213> Physcomitrella patens

<220>

<221> misc_feature

<223> LPAAT

<400> 6

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 acaatatgtg gtcccaagtc atgtgtgtcc cggagggcac taccaccaat ggcagagcaa 180
 taategcctt caaaacagga gcatttttgc ctggtctccc tgtgcagcca atggttatta 240
 gataccctca caagtatgtc aaccctctt ggtgtgacca aggaggtccg ttggtcgttg 300
 ttgtgcagct gatgactcag ttcatcaacc acatggaggt tgaatatattg ccggtcatga 360
 agccaactgt gagagagatg aaataccctc atgaatttgc aagtagagtt cgcagcgaga 420
 tggctaaagc gtaggcacg gtgtgcacag aacacagctt tctggatatt aagctagcgc 480
 tggctgcaga aaagctcaaa cagcctt 507

<210> 7

<211> 1566

<212> DNA

<213> Physcomitrella patens

<220>

<221> CDS

<222> (1)..(1566)

<223> LPAAT

<400> 7

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1 5 10 15	
ctc aac ggg ctc gaa acg cca cta ctg gct gaa ttt cct ctt ggc gaa	96
Leu Asn Gly Leu Glu Thr Pro Leu Leu Ala Glu Phe Pro Leu Gly Glu	
20 25 30	
cgg cct aca ata ggg ccg gag gca cca gta aat ccc ttc cat gaa ccc	144
Arg Pro Thr Ile Gly Pro Glu Ala Pro Val Asn Pro Phe His Glu Pro	
35 40 45	
gat ggt ggt tgg aag acc aac aac gag tgg aat tac ttt caa atg atg	192
Asp Gly Gly Trp Lys Thr Asn Asn Glu Trp Asn Tyr Phe Gln Met Met	
50 55 60	
aaa tcc att ttg ctg att cca ctt ctt ctc gtt cgt cta gtg agc atg	240
Lys Ser Ile Leu Leu Ile Pro Leu Leu Leu Val Arg Leu Val Ser Met	
65 70 75 80	
ata aca atc gta gca ttt gga tat gtg tgg atc agg att tgt ctg atc	288
Ile Thr Ile Val Ala Phe Gly Tyr Val Trp Ile Arg Ile Cys Leu Ile	
85 90 95	
ggc gtc aca gat ccc ttg ttt aag	